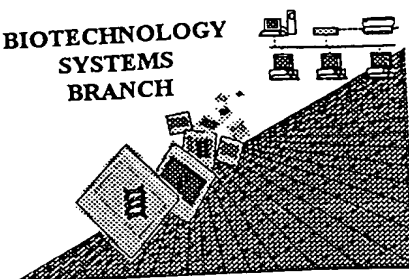


F. Hamud

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/167,705
Art Unit / Team No. : 1646
Date Processed by STIC: 8/31/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/167,705

TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- ___ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- ___ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- ___ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- ___ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- ___ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- ___ Variable Length Sequence(s) ___ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- ___ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- ___ Skipped Sequences (OLD RULES) Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- ___ Skipped Sequences (NEW RULES) Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- ___ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- ___ Use of <213>Organism (NEW RULES) Sequence(s) ___ are missing this mandatory field or its response.
- ___ Use of <220>Feature (NEW RULES) Sequence(s) ___ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- ___ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

F. Hamid

1646

AGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999
TIME: 13:12:04

Input Set: I167705.RAW

This Raw Listing contains the General Information Section and up to first 5 pages. ^{Denotation} ^{Corrected Diskette} ^{Comply} ^{Needed}

1 <110> APPLICANT: Schmidt, Ann Marie
2 Stern, David
3 <120> TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND
4 USES THEREOF
5 <130> FILE REFERENCE: 0575-55873
6 <140> CURRENT APPLICATION NUMBER: US/09/167,705
7 <141> CURRENT FILING DATE: 1998-10-06
8 <160> NUMBER OF SEQ ID NOS: 6
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 395
12 <212> TYPE: DNA
13 <213> ORGANISM: SEQ1
14 <400> SEQUENCE: 1
15 atgactaagc tggaggacca cctggaggga atcatcaaca tcttcacca gtactccgtt 60
16 cgggtggggc atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaaggga 120
17 acttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180
18 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tgggtgtccag 240
19 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttcagca atgttcccaa 300
20 gaagacttac ctttctctc cctgaggctg ctccccgagg gagagagaat tataaacgta 360
21 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395
22 <210> SEQ ID NO 2
23 <211> LENGTH: 50
24 <212> TYPE: PRT
25 <213> ORGANISM: SEQ2
26 <400> SEQUENCE: 2
27 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln
28 1 5 10 15
29 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu
30 20 25 30
31 Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys
32 35 40 45
33 Asp Gln
34 50
35 <210> SEQ ID NO 3
36 <211> LENGTH: 90
37 <212> TYPE: PRT
38 <213> ORGANISM: SEQ3
39 <400> SEQUENCE: 3
40 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
41 1 5 10 15
42 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
43 20 25 30
44 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys

? The only valid responses, per sequence
Rules, are: Artificial Sequence, Unknown, or
Scientific name (Genus/Species)
see circled portion of item 12 on Error summary sheet
see item 10 on Error summary sheet

1646

GE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/167,705

DATE: -09/02/1999
TIME: 13:12:04

Input Set: I167705.RAW

```

45          35          40          45
46      Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
47          50          55          60
48      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
49          65          70          75          80
50      Leu Lys Thr Ala His Ile Asp Ile His Lys
51          85          90
52 <210> SEQ ID NO 4
53 <211> LENGTH: 90
54 <212> TYPE: PRT
55 <213> ORGANISM: SEQ4
56 <400> SEQUENCE: 4
57      Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
58          1          5          10          15
59      Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
60          20          25          30
61      Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
62          35          40          45
63      Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
64          50          55          60
65      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
66          65          70          75          80
67      Leu Lys Thr Ala His Ile Asp Ile His Lys
68          85          90
69 <210> SEQ ID NO 5
70 <211> LENGTH: 18
71 <212> TYPE: PRT
72 <213> ORGANISM: SEQ5
73 <400> SEQUENCE: 5
74      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
75          1          5          10          15
76      Leu Lys
77 <210> SEQ ID NO 6
78 <211> LENGTH: 5
79 <212> TYPE: PRT
80 <213> ORGANISM: SEQ6
81 <400> SEQUENCE: 6
82      Ala Gln Asn Ile Thr
83          1          5

```

PAGE: 3

VERIFICATION SUMMARY
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999
TIME: 13:12:04

Input Set: I167705.RAW

ne ? Error/Warning

Original Text

31 W "N" or "Xaa" used: Feature required

Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys T

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821.825. Applicant's attention is directed to these regulations, published at 114-29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
 For CRF submission help, call (703) 308-4212
 For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.